

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: LABORATOIRES GOEMAR S.A.
- (B) STREET: La Madeleine B.P. 55
- (C) CITY: Saint-Malo
- (E) COUNTRY: France
- (F) POSTAL CODE (ZIP): 35413 Cedex
- (G) TELEPHONE: 99 21 53 70
- (H) TELEFAX: 99 82 56 17

(ii) TITLE OF INVENTION: Glycolyse hydrolase genes and their use for producing enzymes for the biodegradation of carrageenans

(iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2085 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(211..1683, 1880..2083)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AAGCTTTCCG ATTCTATCAT CGAAGTCATA GGAGTGGGTA AACAAAAAAG CATGAAACTA	60
GCTTTTAAAT ATACAGACTT TCAATATAGG TCGCACACAA TATTAACGAA TAAATAAGCA	120

AATCATATAC ATAATCATTG CTTTAAATAT GTTTTAATAC AGATATAAAC ATAGTATGTT 180
 TGTGTTTTTG GTATCTATCG GAGTGAAAAC ATG CGC TTA TAT TTT AGA AAG TTG 234
 Met Arg Leu Tyr Phe Arg Lys Leu
 1 5

TGG TTA ACA AAT TTA TTT TTA GGC GGA GCA CTG GCC TCT TCA GCT GCG 282
 Trp Leu Thr Asn Leu Phe Leu Gly Gly Ala Leu Ala Ser Ser Ala Ala
 10 15 20

ATA GGG GCT GTC TCC CCC AAG ACT TAT AAG GAC GCA GAT TTT TAT GTT 330
 Ile Gly Ala Val Ser Pro Lys Thr Tyr Lys Asp Ala Asp Phe Tyr Val
 25 30 35 40

GCC CCT ACT CAA CAA GAT GTT AAC TAT GAT TTA GTT GAT GAT TTT GGC 378
 Ala Pro Thr Gln Gln Asp Val Asn Tyr Asp Leu Val Asp Asp Phe Gly
 45 50 55

GCT AAT GGA AAC GAC ACT AGT GAT GAC AGT AAT GCT TTA CAA AGA GCA 426
 Ala Asn Gly Asn Asp Thr Ser Asp Asp Ser Asn Ala Leu Gln Arg Ala
 60 65 70

ATT AAT GCT ATT AGT AGA AAA CCG AAT GGG GGC ACT TTA CTA ATA CCG 474
 Ile Asn Ala Ile Ser Arg Lys Pro Asn Gly Gly Thr Leu Leu Ile Pro
 75 80 85

AAT GGA ACT TAC CAT TTC CTC GGC ATA CAG ATG AAG TCG AAC GTA CAC 522
 Asn Gly Thr Tyr His Phe Leu Gly Ile Gln Met Lys Ser Asn Val His
 90 95 100

ATC CGT GTT GAG AGT GAC GTG ATA ATC AAG CCA ACG TGG AAT GGG GAT 570
 Ile Arg Val Glu Ser Asp Val Ile Ile Lys Pro Thr Trp Asn Gly Asp
 105 110 115 120

GGC AAA AAC CAC CGA CTA TTT GAA GTT GGC GTA AAC AAT ATT GTA AGA 618
 Gly Lys Asn His Arg Leu Phe Glu Val Gly Val Asn Asn Ile Val Arg
 125 130 135

AAC TTC AGC TTT CAA GGG TTA GGA AAC GGT TTT TTG GTG GAT TTT AAA 666
 Asn Phe Ser Phe Gln Gly Leu Gly Asn Gly Phe Leu Val Asp Phe Lys
 140 145 150

GAT TCT CGC GAC AAA AAC TTA GCT GTT TTT AAG TTA GGC GAT GTT AGA 714
 Asp Ser Arg Asp Lys Asn Leu Ala Val Phe Lys Leu Gly Asp Val Arg
 155 160 165

AAT TAC AAA ATT TCC AAT TTT ACC ATT GAT GAT AAT AAA ACG ATA TTT Asn Tyr Lys Ile Ser Asn Phe Thr Ile Asp Asp Asn Lys Thr Ile Phe 170 175 180	762
GCC TCA ATT TTA GTG GAC GTA ACA GAA CGT AAT GGG CGG TTA CAT TGG Ala Ser Ile Leu Val Asp Val Thr Glu Arg Asn Gly Arg Leu His Trp 185 190 195 200	810
TCG CGT AAT GGA ATT ATC GAA AGA ATA AAA CAA AAT AAC GCT TTG TTC Ser Arg Asn Gly Ile Ile Glu Arg Ile Lys Gln Asn Asn Ala Leu Phe 205 210 215	858
GGC TAC GGC CTT ATT CAA ACC TAT GGC GCA GAT AAT ATT TTG TTT AGG Gly Tyr Gly Leu Ile Gln Thr Tyr Gly Ala Asp Asn Ile Leu Phe Arg 220 225 230	906
AAC CTC CAT TCG GAA GGC GGA ATT GCG TTA CGG ATG GAA ACT GAC AAC Asn Leu His Ser Glu Gly Gly Ile Ala Leu Arg Met Glu Thr Asp Asn 235 240 245	954
TTA CTT ATG AAA AAT TAT AAG CAA GGC GGA ATA AGA AAC ATC TTT GCT Leu Leu Met Lys Asn Tyr Lys Gln Gly Gly Ile Arg Asn Ile Phe Ala 250 255 260	1002
GAT AAT ATC AGA TGT AGC AAA GGA CTT GCG GCG GTC ATG TTT GGC CCA Asp Asn Ile Arg Cys Ser Lys Gly Leu Ala Ala Val Met Phe Gly Pro 265 270 275 280	1050
CAT TTT ATG AAG AAT GGA GAT GTG CAA GTG ACC AAT GTC AGC TCA GTT His Phe Met Lys Asn Gly Asp Val Gln Val Thr Asn Val Ser Ser Val 285 290 295	1098
AGT TGC GGT TCG GCT GTA CGA AGT GAT AGT GGA TTT GTC GAA CTC TTT Ser Cys Gly Ser Ala Val Arg Ser Asp Ser Gly Phe Val Glu Leu Phe 300 305 310	1146
AGC CCG ACA GAC GAA GTA CAT ACG CGT CAA AGT TGG AAA CAA GCC GTT Ser Pro Thr Asp Glu Val His Thr Arg Gln Ser Trp Lys Gln Ala Val 315 320 325	1194
GAA AGT AAA TTG GGC CGA GGG TGT GCG CAA ACC CCT TAT GCT AGA GGT Glu Ser Lys Leu Gly Arg Gly Cys Ala Gln Thr Pro Tyr Ala Arg Gly 330 335 340	1242

AAT GGT GGT ACA CGG TGG GCG GCT CGC GTA ACA CAA AAA GAC GCG TGT 1290
 Asn Gly Gly Thr Arg Trp Ala Ala Arg Val Thr Gln Lys Asp Ala Cys
 345 350 355 360

TTA GAT AAA GCA AAA CTG GAA TAT GGA ATA GAG CCT GGT TCA TTT GGC 1338
 Leu Asp Lys Ala Lys Leu Glu Tyr Gly Ile Glu Pro Gly Ser Phe Gly
 365 370 375

ACG GTT AAA GTC TTT GAT GTT ACA GCG CGT TTT GGT TAT AAC GCA GAT 1386
 Thr Val Lys Val Phe Asp Val Thr Ala Arg Phe Gly Tyr Asn Ala Asp
 380 385 390

CTT AAA CAG GAC CAG CTA GAC TAC TTT TCT ACA TCC AAC CCT ATG TGC 1434
 Leu Lys Gln Asp Gln Leu Asp Tyr Phe Ser Thr Ser Asn Pro Met Cys
 395 400 405

AAG CGT GTA TGC CTT CCT ACA AAA GAA CAA TGG AGT AAG CAA GGC CAA 1482
 Lys Arg Val Cys Leu Pro Thr Lys Glu Gln Trp Ser Lys Gln Gly Gln
 410 415 420

ATT TAC ATT GGT CCG TCA TTA GCT GCA GTA ATT GAT ACC ACA CCT GAA 1530
 Ile Tyr Ile Gly Pro Ser Leu Ala Ala Val Ile Asp Thr Thr Pro Glu
 425 430 435 440

ACT TCA AAA TAC GAT TAT GAT GTG AAA ACT TTT AAC GTC AAA AGA ATA 1578
 Thr Ser Lys Tyr Asp Tyr Asp Val Lys Thr Phe Asn Val Lys Arg Ile
 445 450 455

AAT TTT CCT GTA AAT TCA CAC AAG ACT ATC GAC ACG AAT ACT GAA AGT 1626
 Asn Phe Pro Val Asn Ser His Lys Thr Ile Asp Thr Asn Thr Glu Ser
 460 465 470

AGC CGT GTC TGC AAT TAT TAC GGT ATG TCC GAA TGC TCC AGC AGT CGA 1674
 Ser Arg Val Cys Asn Tyr Tyr Gly Met Ser Glu Cys Ser Ser Ser Arg
 475 480 485

TGG GAG CGA TAGATTAAGC CGCTATATTC ATTTACTAGG TAAAACTTCA 1723
 Trp Glu Arg
 490

AGCCGCATTC GAAGAACTAT CGAACGCGGC TTTTGTGTTA AGAGCGCCTA TGA CTCAGTA 1783
 TATTTTGTAT AAATATAATT TTACATCTTG TTAAAGTAAA CATCATATGT TTATATAGGT 1843
 GCAATCTAAT TTGTTAATAT AGTGTGGAG ATAGGT ATG AAA GGT GTT TCT ACG 1897
 Met Lys Gly Val Ser Thr
 495

GAA GTG CCT GTA TCA ATT GAA GTT ATT CAA GGC GAC CTT CTA GA 2085
Glu Val Pro Val Ser Ile Glu Val Ile Gln Gly Asp Leu Leu
550 555

Met	Arg	Leu	Tyr	Phe	Arg	Lys	Leu	Trp	Leu	Thr	Asn	Leu	Phe	Leu	Gly
1				5					10					15	
Gly	Ala	Leu	Ala	Ser	Ser	Ala	Ala	Ile	Gly	Ala	Val	Ser	Pro	Lys	Thr
			20					25					30		
Tyr	Lys	Asp	Ala	Asp	Phe	Tyr	Val	Ala	Pro	Thr	Gln	Gln	Asp	Val	Asn
		35					40					45			
Tyr	Asp	Leu	Val	Asp	Asp	Phe	Gly	Ala	Asn	Gly	Asn	Asp	Thr	Ser	Asp
	50					55					60				
Asp	Ser	Asn	Ala	Leu	Gln	Arg	Ala	Ile	Asn	Ala	Ile	Ser	Arg	Lys	Pro
65					70					75				80	
Asn	Gly	Gly	Thr	Leu	Leu	Ile	Pro	Asn	Gly	Thr	Tyr	His	Phe	Leu	Gly
				85					90					95	
Ile	Gln	Met	Lys	Ser	Asn	Val	His	Ile	Arg	Val	Glu	Ser	Asp	Val	Ile
			100					105					110		
Ile	Lys	Pro	Thr	Trp	Asn	Gly	Asp	Gly	Lys	Asn	His	Arg	Leu	Phe	Glu
		115					120					125			
Val	Gly	Val	Asn	Asn	Ile	Val	Arg	Asn	Phe	Ser	Phe	Gln	Gly	Leu	Gly
	130					135					140				

Asn	Gly	Phe	Leu	Val	Asp	Phe	Lys	Asp	Ser	Arg	Asp	Lys	Asn	Leu	Ala
145					150					155					160
Val	Phe	Lys	Leu	Gly	Asp	Val	Arg	Asn	Tyr	Lys	Ile	Ser	Asn	Phe	Thr
				165					170					175	
Ile	Asp	Asp	Asn	Lys	Thr	Ile	Phe	Ala	Ser	Ile	Leu	Val	Asp	Val	Thr
				180					185					190	
Glu	Arg	Asn	Gly	Arg	Leu	His	Trp	Ser	Arg	Asn	Gly	Ile	Ile	Glu	Arg
			195						200				205		
Ile	Lys	Gln	Asn	Asn	Ala	Leu	Phe	Gly	Tyr	Gly	Leu	Ile	Gln	Thr	Tyr
		210				215					220				
Gly	Ala	Asp	Asn	Ile	Leu	Phe	Arg	Asn	Leu	His	Ser	Glu	Gly	Gly	Ile
225					230					235					240
Ala	Leu	Arg	Met	Glu	Thr	Asp	Asn	Leu	Leu	Met	Lys	Asn	Tyr	Lys	Gln
				245					250					255	
Gly	Gly	Ile	Arg	Asn	Ile	Phe	Ala	Asp	Asn	Ile	Arg	Cys	Ser	Lys	Gly
			260						265					270	
Leu	Ala	Ala	Val	Met	Phe	Gly	Pro	His	Phe	Met	Lys	Asn	Gly	Asp	Val
			275						280				285		
Gln	Val	Thr	Asn	Val	Ser	Ser	Val	Ser	Cys	Gly	Ser	Ala	Val	Arg	Ser
		290				295						300			
Asp	Ser	Gly	Phe	Val	Glu	Leu	Phe	Ser	Pro	Thr	Asp	Glu	Val	His	Thr
305					310						315				320
Arg	Gln	Ser	Trp	Lys	Gln	Ala	Val	Glu	Ser	Lys	Leu	Gly	Arg	Gly	Cys
				325						330				335	
Ala	Gln	Thr	Pro	Tyr	Ala	Arg	Gly	Asn	Gly	Gly	Thr	Arg	Trp	Ala	Ala
			340						345					350	
Arg	Val	Thr	Gln	Lys	Asp	Ala	Cys	Leu	Asp	Lys	Ala	Lys	Leu	Glu	Tyr
			355					360				365			
Gly	Ile	Glu	Pro	Gly	Ser	Phe	Gly	Thr	Val	Lys	Val	Phe	Asp	Val	Thr
		370				375						380			
Ala	Arg	Phe	Gly	Tyr	Asn	Ala	Asp	Leu	Lys	Gln	Asp	Gln	Leu	Asp	Tyr
385					390					395					400
Phe	Ser	Thr	Ser	Asn	Pro	Met	Cys	Lys	Arg	Val	Cys	Leu	Pro	Thr	Lys
				405					410					415	
Glu	Gln	Trp	Ser	Lys	Gln	Gly	Gln	Ile	Tyr	Ile	Gly	Pro	Ser	Leu	Ala
			420					425					430		
Ala	Val	Ile	Asp	Thr	Thr	Pro	Glu	Thr	Ser	Lys	Tyr	Asp	Tyr	Asp	Val
			435					440				445			
Lys	Thr	Phe	Asn	Val	Lys	Arg	Ile	Asn	Phe	Pro	Val	Asn	Ser	His	Lys
		450				455						460			
Thr	Ile	Asp	Thr	Asn	Thr	Glu	Ser	Ser	Arg	Val	Cys	Asn	Tyr	Tyr	Gly
465					470					475					480
Met	Ser	Glu	Cys	Ser	Ser	Ser	Arg	Trp	Glu	Arg	Met	Lys	Gly	Val	Ser
				485					490					495	
Thr	Lys	Asn													

Gln Ser Val Ser Ala Gln Glu Ala Lys Gln Pro Glu Lys Glu Glu Lys
 515 520 525
 Asp Val Glu Val Ile Leu Val Ser Ala Gln Lys Arg Glu Gln Ala Leu
 530 535 540
 Lys Glu Val Pro Val Ser Ile Glu Val Ile Gln Gly Asp Leu Leu
 545 550 555

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1997 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(333..1805, 1866..1997)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCCTAAAAAC TATTCTTCAT ACCCTTTGAT GTATACGTTT AAACATATAGG GAGTTAATCT 60
 GGTTTTGGTG CAATTCTAGT TTAATAAATG AAGCCTTCTT TTTTGACTTA CATTTTATTA 120
 ACCTCTTGAA TTCTTGGGGC TTGCTAATTA TAAAATACTT AATATCAGGT GGTTGTGTAA 180
 AAGAGGTGGA AGGGTATAGG ACCGTTACTT ATAATTGGCC CCTGTCGGAA GGGGGGTTAA 240
 AGGTAAAATA GTGTTTAAGT GTATTAATTA ACTTCTATAT AAGTAGGAAA ATACACTATA 300
 TATTGCGACA TTATTAACCT TAAATTCTTA CA ATG AAA TTA CAA TTT AAA CCT 353
 Met Lys Leu Gln Phe Lys Pro
 1 5

GTT TAT TTA GCG TCA ATT GCC ATA ATG GCA ATA GGA TGC ACC AAA GAA 401
 Val Tyr Leu Ala Ser Ile Ala Ile Met Ala Ile Gly Cys Thr Lys Glu
 10 15 20

GTG ACG GAA AAC GAT ACC TCC GAA ATT TCG GAA GTT CCA ACT GAA TTG 449
 Val Thr Glu Asn Asp Thr Ser Glu Ile Ser Glu Val Pro Thr Glu Leu
 25 30 35

AGG GCC GCG GCT TCT TCA TTT TAT ACC CCA CCG GGT CAG AAT GTA CGG 497
 Arg Ala Ala Ala Ser Ser Phe Tyr Thr Pro Pro Gly Gln Asn Val Arg
 40 45 50 55

GCC AAT AAA AAA AAC CTG GTC ACG GAT TAC GGT GTT AAC CAC AAT GAT 545
 Ala Asn Lys Lys Asn Leu Val Thr Asp Tyr Gly Val Asn His Asn Asp
 60 65 70

CAG AAC GAT GAT AGT AGC AAA TTA AAC CTG GCT ATC AAA GAT TTA TCG 593
 Gln Asn Asp Asp Ser Ser Lys Leu Asn Leu Ala Ile Lys Asp Leu Ser
 75 80 85

GAT ACC GGT GGT ATA CTG ACC CTT CCT AAG GGA AAG TAC TAT TTG ACC 641
 Asp Thr Gly Gly Ile Leu Thr Leu Pro Lys Gly Lys Tyr Tyr Leu Thr
 90 95 100

AAA ATT AGA ATG CGC TCT AAT GTA CAT CTT GAA ATA GAA AAG GGA ACG 689
 Lys Ile Arg Met Arg Ser Asn Val His Leu Glu Ile Glu Lys Gly Thr
 105 110 115

GTA ATC TAT CCG ACC AAG GGG TTG ACT CCT GCG AAG AAT CAC AGA ATT 737
 Val Ile Tyr Pro Thr Lys Gly Leu Thr Pro Ala Lys Asn His Arg Ile
 120 125 130 135

TTT GAT TTT GCC AGT AAA ACA GAG GAA AAA ATA GAA AAC GCC AGT ATA 785
 Phe Asp Phe Ala Ser Lys Thr Glu Glu Lys Ile Glu Asn Ala Ser Ile
 140 145 150

GTG GGT AAA GGA GGT AAG TTT ATA GTA GAC CTA AGA GGC AAC AGT TCT 833
 Val Gly Lys Gly Gly Lys Phe Ile Val Asp Leu Arg Gly Asn Ser Ser
 155 160 165

AAA AAC CAA ATT GTA GCC GAT GTT GGT AAC GTA ACC AAC TTT AAA ATA 881
 Lys Asn Gln Ile Val Ala Asp Val Gly Asn Val Thr Asn Phe Lys Ile
 170 175 180

TCG AAT TTT ACG ATC AAG GAT GAA AAA ACC ATC TTT GCT TCG ATA TTG 929
 Ser Asn Phe Thr Ile Lys Asp Glu Lys Thr Ile Phe Ala Ser Ile Leu
 185 190 195

GTA AGC TTT ACG GAT AAG GCA GGC AAT GCT TGG CCA CAT AAA GGT ATT 977
 Val Ser Phe Thr Asp Lys Ala Gly Asn Ala Trp Pro His Lys Gly Ile
 200 205 210 215

ATT GAG AAT ATA GAC CAG GCG AAT GCC CAT ACG GGA TAT GGC CTC ATA 1025
 Ile Glu Asn Ile Asp Gln Ala Asn Ala His Thr Gly Tyr Gly Leu Ile
 220 225 230

CAG GCG TAC GCG GCA GAT AAC ATT CTG TTC AAC AAT CTA AGT TGT ACG	1073
Gln Ala Tyr Ala Ala Asp Asn Ile Leu Phe Asn Asn Leu Ser Cys Thr	
235 240 245	
GGC GGG GTA ACC TTG CGT TTA GAA ACC GAC AAC CTC GCT ATG AAA ACC	1121
Gly Gly Val Thr Leu Arg Leu Glu Thr Asp Asn Leu Ala Met Lys Thr	
250 255 260	
GCT AAA AAA GGG GGG GTA AGG GAT ATT TTT GCC ACA AAG ATC AAG AAT	1169
Ala Lys Lys Gly Gly Val Arg Asp Ile Phe Ala Thr Lys Ile Lys Asn	
265 270 275	
ACC AAT GGC TTG ACC CCG GTA ATG TTC TCT CCC CAT TTT ATG GAA AAC	1217
Thr Asn Gly Leu Thr Pro Val Met Phe Ser Pro His Phe Met Glu Asn	
280 285 290 295	
GGT AAA GTG ACC ATA GAT GAT GTA ACC GCC ATC GGT TGT GCA TAT GCC	1265
Gly Lys Val Thr Ile Asp Asp Val Thr Ala Ile Gly Cys Ala Tyr Ala	
300 305 310	
GTA CGT GTA GAG CAC GGT TTT ATA GAG ATT TTC GAT AAG GGG AAT AGG	1313
Val Arg Val Glu His Gly Phe Ile Glu Ile Phe Asp Lys Gly Asn Arg	
315 320 325	
GCA AGT GCC GAC GCT TTC AAG AAC TAT ATT GAA GGT ATT CTA GGA GCT	1361
Ala Ser Ala Asp Ala Phe Lys Asn Tyr Ile Glu Gly Ile Leu Gly Ala	
330 335 340	
GGC TCG GTA GAA GTC GTG TAC AAA CGT AAT AAC GGA AGA ACA TGG GCG	1409
Gly Ser Val Glu Val Val Tyr Lys Arg Asn Asn Gly Arg Thr Trp Ala	
345 350 355	
GCA CGT ATC GCA AAC GAC TTT AAC GAA GCG GCG TAT AAC CAC TCC AAT	1457
Ala Arg Ile Ala Asn Asp Phe Asn Glu Ala Ala Tyr Asn His Ser Asn	
360 365 370 375	
CCT GCC GTT AGC GGA ATC AAA CCA GGG AAA TTC GCC ACA TCT AAG GTA	1505
Pro Ala Val Ser Gly Ile Lys Pro Gly Lys Phe Ala Thr Ser Lys Val	
380 385 390	
ACC AAT GTT AAG GCA ACC TAT AAG GGT ACT GGC GCC AAA CTC AAG CAG	1553
Thr Asn Val Lys Ala Thr Tyr Lys Gly Thr Gly Ala Lys Leu Lys Gln	
395 400 405	

GCA TTC TTA TCC TAT TTA CCC TGT TCG GAA CGT TCT AAG GTT TGT CGG 1601
 Ala Phe Leu Ser Tyr Leu Pro Cys Ser Glu Arg Ser Lys Val Cys Arg
 410 415 420

CCA GGT CCA GAT GGG TTC GAG TAT AAC GGA CCC TCC TTG GGA GTT ACC 1649
 Pro Gly Pro Asp Gly Phe Glu Tyr Asn Gly Pro Ser Leu Gly Val Thr
 425 430 435

ATC GAT AAC ACG AAA AGG GAC AAC AGC CTT GGC AAT TAT AAC GTC AAT 1697
 Ile Asp Asn Thr Lys Arg Asp Asn Ser Leu Gly Asn Tyr Asn Val Asn
 440 445 450 455

GTA AGC ACC TCC AGT GTT CAG GGC TTT CCC AAT AAT TAC GTT TTA AAC 1745
 Val Ser Thr Ser Ser Val Gln Gly Phe Pro Asn Asn Tyr Val Leu Asn
 460 465 470

GTA AAG TAT AAT ACC CCT AAA GTA TGT AAC CAA AAT CTA GGT AGT ATT 1793
 Val Lys Tyr Asn Thr Pro Lys Val Cys Asn Gln Asn Leu Gly Ser Ile
 475 480 485

ACT TCG TGT AAC TGATCACGAA ACAATTTGTA AATAAAAAGC AGCTGTCCCT 1845
 Thr Ser Cys Asn
 490

TATTACGGGC GGCTGCTTTT ATG TCT TTA AGC CAT GTC GTG ATT TAT TGG 1895
 Met Ser Leu Ser His Val Val Ile Tyr Trp
 495 500

CGA CTT TTG ATA AAG GCT TGG ATT TCT TCC GGG GTA AAT ATC GGA TTG 1943
 Arg Leu Leu Ile Lys Ala Trp Ile Ser Ser Gly Val Asn Ile Gly Leu
 505 510 515

GCC CCT TCC CTA CCG GCT ACC ATA GCT CTA TGC TCC TAT GCA CAG GCG 1991
 Ala Pro Ser Leu Pro Ala Thr Ile Ala Leu Cys Ser Tyr Ala Gln Ala
 520 525 530

AAA TCT 1997
 Lys Ser
 535

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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Met Lys Leu Gln Phe Lys Pro Val Tyr Leu Ala Ser Ile Ala Ile Met
 1           5           10           15
Ala Ile Gly Cys Thr Lys Glu Val Thr Glu Asn Asp Thr Ser Glu Ile
      20           25           30
Ser Glu Val Pro Thr Glu Leu Arg Ala Ala Ala Ser Ser Phe Tyr Thr
      35           40           45
Pro Pro Gly Gln Asn Val Arg Ala Asn Lys Lys Asn Leu Val Thr Asp
      50           55           60
Tyr Gly Val Asn His Asn Asp Gln Asn Asp Asp Ser Ser Lys Leu Asn
      65           70           75           80
Leu Ala Ile Lys Asp Leu Ser Asp Thr Gly Gly Ile Leu Thr Leu Pro
      85           90           95
Lys Gly Lys Tyr Tyr Leu Thr Lys Ile Arg Met Arg Ser Asn Val His
      100           105           110
Leu Glu Ile Glu Lys Gly Thr Val Ile Tyr Pro Thr Lys Gly Leu Thr
      115           120           125
Pro Ala Lys Asn His Arg Ile Phe Asp Phe Ala Ser Lys Thr Glu Glu
      130           135           140
Lys Ile Glu Asn Ala Ser Ile Val Gly Lys Gly Gly Lys Phe Ile Val
      145           150           155           160
Asp Leu Arg Gly Asn Ser Ser Lys Asn Gln Ile Val Ala Asp Val Gly
      165           170           175
Asn Val Thr Asn Phe Lys Ile Ser Asn Phe Thr Ile Lys Asp Glu Lys
      180           185           190
Thr Ile Phe Ala Ser Ile Leu Val Ser Phe Thr Asp Lys Ala Gly Asn
      195           200           205
Ala Trp Pro His Lys Gly Ile Ile Glu Asn Ile Asp Gln Ala Asn Ala
      210           215           220
His Thr Gly Tyr Gly Leu Ile Gln Ala Tyr Ala Ala Asp Asn Ile Leu
      225           230           235           240
Phe Asn Asn Leu Ser Cys Thr Gly Gly Val Thr Leu Arg Leu Glu Thr
      245           250           255
Asp Asn Leu Ala Met Lys Thr Ala Lys Lys Gly Gly Val Arg Asp Ile
      260           265           270
Phe Ala Thr Lys Ile Lys Asn Thr Asn Gly Leu Thr Pro Val Met Phe
      275           280           285
Ser Pro His Phe Met Glu Asn Gly Lys Val Thr Ile Asp Asp Val Thr
      290           295           300
Ala Ile Gly Cys Ala Tyr Ala Val Arg Val Glu His Gly Phe Ile Glu
      305           310           315           320

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Ile Phe Asp Lys Gly Asn Arg Ala Ser Ala Asp Ala Phe Lys Asn Tyr
      325                      330                      335
Ile Glu Gly Ile Leu Gly Ala Gly Ser Val Glu Val Val Tyr Lys Arg
      340                      345                      350
Asn Asn Gly Arg Thr Trp Ala Ala Arg Ile Ala Asn Asp Phe Asn Glu
      355                      360                      365
Ala Ala Tyr Asn His Ser Asn Pro Ala Val Ser Gly Ile Lys Pro Gly
      370                      375                      380
Lys Phe Ala Thr Ser Lys Val Thr Asn Val Lys Ala Thr Tyr Lys Gly
385                      390                      395                      400
Thr Gly Ala Lys Leu Lys Gln Ala Phe Leu Ser Tyr Leu Pro Cys Ser
      405                      410                      415
Glu Arg Ser Lys Val Cys Arg Pro Gly Pro Asp Gly Phe Glu Tyr Asn
      420                      425                      430
Gly Pro Ser Leu Gly Val Thr Ile Asp Asn Thr Lys Arg Asp Asn Ser
      435                      440                      445
Leu Gly Asn Tyr Asn Val Asn Val Ser Thr Ser Ser Val Gln Gly Phe
      450                      455                      460
Pro Asn Asn Tyr Val Leu Asn Val Lys Tyr Asn Thr Pro Lys Val Cys
465                      470                      475                      480
Asn Gln Asn Leu Gly Ser Ile Thr Ser Cys Asn Met Ser Leu Ser His
      485                      490                      495
Val Val Ile Tyr Trp Arg Leu Leu Ile Lys Ala Trp Ile Ser Ser Gly
      500                      505                      510
Val Asn Ile Gly Leu Ala Pro Ser Leu Pro Ala Thr Ile Ala Leu Cys
      515                      520                      525
Ser Tyr Ala Gln Ala Lys Ser
      530                      535

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1..498, 741..1931, 2009..2179)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CATTTT TAGA GAACAGTAAA ACCATTTTTT GAGGTTTGGT GTTGTATATA AATATTAAAT 588

ATCCCCACTC GCTCAGCTTT TTTTGTGCGA GTTGTGAGAA TTAGCTTAAC AGGTAAGGTT	648
TACGTATCTG TATATCTAAA CTCTTCGAAT ATAACACTGT ATCTGTTGCT GAGCTGTGGC	708
TCAGTTCACA CTAACAAAGG ATGGATAAAT AA ATG AAA CCT ATA AGT ATT GTG	761
Met Lys Pro Ile Ser Ile Val	
170	
GCA TTC CCT ATA CCA GCT ATA AGT ATG CTT CTT TTA AGT GCA GTA TCA	809
Ala Phe Pro Ile Pro Ala Ile Ser Met Leu Leu Leu Ser Ala Val Ser	
175 180 185	
CAA GCA GCA TCT ATG CAA CCT CCC ATC GCA AAA CCT GGT GAA ACA TGG	857
Gln Ala Ala Ser Met Gln Pro Pro Ile Ala Lys Pro Gly Glu Thr Trp	
190 195 200 205	
ATT TTA CAA GCC AAA CGC TCT GAC GAA TTT AAC GTA AAA GAT GCG ACA	905
Ile Leu Gln Ala Lys Arg Ser Asp Glu Phe Asn Val Lys Asp Ala Thr	
210 215 220	
AAG TGG AAC TTT CAA ACA GAA AAC TAT GGG GTA TGG TCT TGG AAA AAT	953
Lys Trp Asn Phe Gln Thr Glu Asn Tyr Gly Val Trp Ser Trp Lys Asn	
225 230 235	
GAA AAT GCG ACA GTA TCT AAT GGC AAA CTA AAA TTA ACC ACT AAG CGA	1001
Glu Asn Ala Thr Val Ser Asn Gly Lys Leu Lys Leu Thr Thr Lys Arg	
240 245 250	
GAA TCT CAT CAA CGT ACA TTC TGG GAT GGC TGT AAT CAG CAG CAA GTT	1049
Glu Ser His Gln Arg Thr Phe Trp Asp Gly Cys Asn Gln Gln Gln Val	
255 260 265	
GCA AAT TAC CCA CTT TAT TAT ACA TCG GGT GTC GCT AAA TCC AGA GCT	1097
Ala Asn Tyr Pro Leu Tyr Tyr Thr Ser Gly Val Ala Lys Ser Arg Ala	
270 275 280 285	
ACA GGT AAT TAT GGC TAT TAC GAA GCT CGA ATC AAA GGA GCG AGT ACA	1145
Thr Gly Asn Tyr Gly Tyr Tyr Glu Ala Arg Ile Lys Gly Ala Ser Thr	
290 295 300	
TTT CCT GGC GTA TCG CCT GCT TTT TGG ATG TAT AGC ACC ATT GAC CGT	1193
Phe Pro Gly Val Ser Pro Ala Phe Trp Met Tyr Ser Thr Ile Asp Arg	
305 310 315	
TCA TTA ACG AAA GAA GGG GAT GTC CAA TAT AGC GAA ATA GAC GTA GTG	1241
Ser Leu Thr Lys Glu Gly Asp Val Gln Tyr Ser Glu Ile Asp Val Val	
320 325 330	

GAA CTT ACT CAA AAA AGT GCA GTG AGA GAG TCT GAT CAT GAC TTA CAC	1289
Glu Leu Thr Gln Lys Ser Ala Val Arg Glu Ser Asp His Asp Leu His	
335 340 345	
AAT ATT GTA GTA AAA AAT GGA AAA CCA ACA TGG ATG CGT CCA GGG TCT	1337
Asn Ile Val Val Lys Asn Gly Lys Pro Thr Trp Met Arg Pro Gly Ser	
350 355 360 365	
TTT CCG CAG ACA AAT CAT AAC GGA TAC CAT CTA CCT TTC GAT CCT CGA	1385
Phe Pro Gln Thr Asn His Asn Gly Tyr His Leu Pro Phe Asp Pro Arg	
370 375 380	
AAT GAC TTT CAC ACC TAT GGT GTC AAT GTA ACT AAA GAC AAG ATC ACT	1433
Asn Asp Phe His Thr Tyr Gly Val Asn Val Thr Lys Asp Lys Ile Thr	
385 390 395	
TGG TAC GTA GAT GGT GAA ATT GTG GGC GAA AAG GAT AAC TTA TAC TGG	1481
Trp Tyr Val Asp Gly Glu Ile Val Gly Glu Lys Asp Asn Leu Tyr Trp	
400 405 410	
CAT CGT CAA ATG AAT CTC ACA TTA TCA CAA GGC TTA CGC GCG CCG CAT	1529
His Arg Gln Met Asn Leu Thr Leu Ser Gln Gly Leu Arg Ala Pro His	
415 420 425	
ACA CAA TGG AAA TGT AAT CAA TTT TAC CCA TCA GCG AAT AAA TCA GCA	1577
Thr Gln Trp Lys Cys Asn Gln Phe Tyr Pro Ser Ala Asn Lys Ser Ala	
430 435 440 445	
GAA GGC TTC CCA ACA TCA ATG GAA GTT GAT TAT GTA AGA ACG TGG GTA	1625
Glu Gly Phe Pro Thr Ser Met Glu Val Asp Tyr Val Arg Thr Trp Val	
450 455 460	
AAG GTG GGC AAT AAC AAC TCT GCT CCA GGC GAG GGG CAG TCA TGT CCT	1673
Lys Val Gly Asn Asn Asn Ser Ala Pro Gly Glu Gly Gln Ser Cys Pro	
465 470 475	
AAC ACG TTT GTA GCT GTC AAT AGT GTT CAA CTA AGC GCA GCA AAA CAA	1721
Asn Thr Phe Val Ala Val Asn Ser Val Gln Leu Ser Ala Ala Lys Gln	
480 485 490	
ACA CTT CGA AAG GGC CAA TCT ACA ACG CTA GAA AGC ACA GTT CTT CCA	1769
Thr Leu Arg Lys Gly Gln Ser Thr Thr Leu Glu Ser Thr Val Leu Pro	
495 500 505	

AAC TGT GCA ACC AAC AAG AAA GTC ATT TAT TCA TCA AGC AAT AAA AAT 1817
Asn Cys Ala Thr Asn Lys Lys Val Ile Tyr Ser Ser Ser Asn Lys Asn
510 515 520 525

GTG GCA ACT GTG AAC AGT GCT GGC GTT GTA AAA GCT AAA AAT AAA GGC 1865
Val Ala Thr Val Asn Ser Ala Gly Val Val Lys Ala Lys Asn Lys Gly
530 535 540

ACT GCG ACG ATT ACG GTT AAA ACT AAA AAC AAA GGG AAA ATA GAT AAA 1913
Thr Ala Thr Ile Thr Val Lys Thr Lys Asn Lys Gly Lys Ile Asp Lys
545 550 555

TTA ACC ATT GCG GTG AAT TAAGCTAACT CAACTAGCC TCGAAGGATT 1961
Leu Thr Ile Ala Val Asn
560

GAGGCACTTT ATTTATAGGT CTCAGGCTTC GACTTTTTGG AGGGGGT ATG AAA AAG 2017
Met Lys Lys
565

GTA AAT TTA TCC AGC AAG TGG ATA ATT AGC ATT AGT TTA CTA ATC ATT 2065
Val Asn Leu Ser Ser Lys Trp Ile Ile Ser Ile Ser Leu Leu Ile Ile
570 575 580

TGT GAT TAT GTT TAT TTA ATA CGA ACA AAC GTT AAC GAG CAA GCT AAC 2113
Cys Asp Tyr Val Tyr Leu Ile Arg Thr Asn Val Asn Glu Gln Ala Asn
585 590 595

GCA GAA GCT ACT GCA CAT ATG CAT TAC AAA ATA AAT AAT ACG AAA CAC 2161
Ala Glu Ala Thr Ala His Met His Tyr Lys Ile Asn Asn Thr Lys His
600 605 610

TCA AAA GGA AAG CTT GAT C 2180
Ser Lys Gly Lys Leu Asp
615 620

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Asp	His	Ile	Ile	Pro	Leu	Gln	Ile	Lys	Asn	Ser	Gln	Asp	Ser	Gln	Ile
1				5					10					15	
Ile	Ser	Phe	Phe	Lys	Ala	Asp	Lys	Gly	Ser	Val	Ser	Arg	Gln	Val	His
			20					25					30		
Pro	Pro	Trp	Pro	Val	Pro	Cys	Lys	Ser	Lys	Leu	Gln	Glu	Gln	Asp	Ser
		35					40					45			
Ser	Glu	Ser	Lys	Glu	Ser	Lys	Ala	Glu	Gln	Val	Lys	Ile	Asn	Asn	Cys
	50					55				60					
Val	Val	Gln	Asn	Ala	Met	Leu	Tyr	Ile	Glu	Asn	Asn	Tyr	Phe	Asn	Asp
65				70						75					80
Ile	Asn	Ile	Asp	Thr	Val	Ala	Phe	Ser	Val	Gly	Val	Ser	Arg	Ser	Tyr
				85					90					95	
Leu	Val	Lys	Gln	Phe	Lys	Leu	Ala	Thr	Asn	Lys	Thr	Ile	Asn	Asn	Arg
			100					105					110		
Ile	Ile	Glu	Val	Arg	Ile	Glu	Gln	Ala	Lys	Lys	Val	Leu	Leu	Lys	Lys
		115					120					125			
Ser	Val	Thr	Glu	Thr	Ala	Tyr	Glu	Val	Gly	Phe	Asn	Asn	Ser	Asn	Tyr
	130					135					140				
Phe	Ala	Thr	Val	Phe	Lys	Lys	Arg	Thr	Asn	Tyr	Thr	Pro	Lys	Gln	Phe
145					150					155					160
Lys	Arg	Thr	Phe	Ser	Ser	Met	Lys	Pro	Ile	Ser	Ile	Val	Ala	Phe	Pro
				165					170					175	
Ile	Pro	Ala	Ile	Ser	Met	Leu	Leu	Leu	Ser	Ala	Val	Ser	Gln	Ala	Ala
			180					185					190		
Ser	Met	Gln	Pro	Pro	Ile	Ala	Lys	Pro	Gly	Glu	Thr	Trp	Ile	Leu	Gln
		195					200					205			
Ala	Lys	Arg	Ser	Asp	Glu	Phe	Asn	Val	Lys	Asp	Ala	Thr	Lys	Trp	Asn
	210					215					220				
Phe	Gln	Thr	Glu	Asn	Tyr	Gly	Val	Trp	Ser	Trp	Lys	Asn	Glu	Asn	Ala
225					230					235					240
Thr	Val	Ser	Asn	Gly	Lys	Leu	Lys	Leu	Thr	Thr	Lys	Arg	Glu	Ser	His
				245					250					255	
Gln	Arg	Thr	Phe	Trp	Asp	Gly	Cys	Asn	Gln	Gln	Gln	Val	Ala	Asn	Tyr
			260					265					270		
Pro	Leu	Tyr	Tyr	Thr	Ser	Gly	Val	Ala	Lys	Ser	Arg	Ala	Thr	Gly	Asn
		275					280					285			
Tyr	Gly	Tyr	Tyr	Glu	Ala	Arg	Ile	Lys	Gly	Ala	Ser	Thr	Phe	Pro	Gly
	290					295					300				
Val	Ser	Pro	Ala	Phe	Trp	Met	Tyr	Ser	Thr	Ile	Asp	Arg	Ser	Leu	Thr
305					310					315					320
Lys	Glu	Gly	Asp	Val	Gln	Tyr	Ser	Glu	Ile	Asp	Val	Val	Glu	Leu	Thr
				325					330					335	
Gln	Lys	Ser	Ala	Val	Arg	Glu	Ser	Asp	His	Asp	Leu	His	Asn	Ile	Val
			340					345					350		

Val Lys Asn Gly Lys Pro Thr Trp Met Arg Pro Gly Ser Phe Pro Gln
 355 360 365
 Thr Asn His Asn Gly Tyr His Leu Pro Phe Asp Pro Arg Asn Asp Phe
 370 375 380
 His Thr Tyr Gly Val Asn Val Thr Lys Asp Lys Ile Thr Trp Tyr Val
 385 390 395 400
 Asp Gly Glu Ile Val Gly Glu Lys Asp Asn Leu Tyr Trp His Arg Gln
 405 410 415
 Met Asn Leu Thr Leu Ser Gln Gly Leu Arg Ala Pro His Thr Gln Trp
 420 425 430
 Lys Cys Asn Gln Phe Tyr Pro Ser Ala Asn Lys Ser Ala Glu Gly Phe
 435 440 445
 Pro Thr Ser Met Glu Val Asp Tyr Val Arg Thr Trp Val Lys Val Gly
 450 455 460
 Asn Asn Asn Ser Ala Pro Gly Glu Gly Gln Ser Cys Pro Asn Thr Phe
 465 470 475 480
 Val Ala Val Asn Ser Val Gln Leu Ser Ala Ala Lys Gln Thr Leu Arg
 485 490 495
 Lys Gly Gln Ser Thr Thr Leu Glu Ser Thr Val Leu Pro Asn Cys Ala
 500 505 510
 Thr Asn Lys Lys Val Ile Tyr Ser Ser Ser Asn Lys Asn Val Ala Thr
 515 520 525
 Val Asn Ser Ala Gly Val Val Lys Ala Lys Asn Lys Gly Thr Ala Thr
 530 535 540
 Ile Thr Val Lys Thr Lys Asn Lys Gly Lys Ile Asp Lys Leu Thr Ile
 545 550 555 560
 Ala Val Asn Met Lys Lys Val Asn Leu Ser Ser Lys Trp Ile Ile Ser
 565 570 575
 Ile Ser Leu Leu Ile Ile Cys Asp Tyr Val Tyr Leu Ile Arg Thr Asn
 580 585 590
 Val Asn Glu Gln Ala Asn Ala Glu Ala Thr Ala His Met His Tyr Lys
 595 600 605
 Ile Asn Asn Thr Lys His Ser Lys Gly Lys Leu Asp
 610 615 620

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:875..2509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCCTCCGTAT TCGACAATGT TGTACGATGC TTGGCGATTC GGACTCTGTT TAAGCACTCG	60
ATTTCGTAAA GGCACATATCC ACTCATTCAT TCCGACTCAA TATTCTTTTC GACAAATGCA	120
ACCGGTTCCA TTGAAAAGGC CCTAAAAATA CAGCTTTCCC GCCCCCATC GTAGAAGGTT	180
CCAATATGCT TCAACCCCTT TTTCAGCCTT ACTTCAGGGG TATTACTTTC ATGCCTAGGG	240
CCGCAAATAC ATTGCGTTGG ACCCAGTCAC CTATATAATT GAATACGGAA CTACCCATGG	300
CTTCCTTCCC TTTGGGAACC TATGGTACAG ACTTGCCTTT TTAAACCGG TTAATTTCAGC	360
TAATTCGCCA AGCTGGTTCC TTCATAACCT TTGGCCCCGAA ACACCTTGCA AGCACATAAA	420
TCTTATCCAA TATTTTGC GG TCTCATGGGA CAAATCTATA ACAAACATTC AATTTTACCA	480
AACGTTCCGGT AATAAATCTA GTCAAAAACG GGGTCCGATT CATTTTAGAA GAAAGGTAAA	540
GCCCCAAAA GAGCGGTTTA CTTGAAGATA TGATTTATAA AACACAATAA GTGACAAAGG	600
AAGATCATGG CTATAATTAG TTGAAAAAAC AGGGCTTACC ATGACATGGA GCTTTATTGA	660
AAACAGATGT CCAACAAGAA TAAAGGAGGG CCGTTCGACC GCGACGTTTA AATAAAAACA	720
TATTCATAT CAAAATTTAA TTAAGGTTCT TTCCTACAGT ATTTATAAGA AATTACTAAA	780
ATTAGTTAGG ATAATACTAC AAAATGGTAA AATTGGATTA CTCAGATTGA ACCATAGCCT	840
CTACTTTAGT CGGCTAACAA AAACAATTAT AGTA ATG AAA AAA CCA AAT TTT	892
Met Lys Lys Pro Asn Phe	
1 5	
TAT GGC AAG ATG GGT AGA ACT GCA CTT TCA AGT CTT TTC TAC CTC TTT	940
Tyr Gly Lys Met Gly Arg Thr Ala Leu Ser Ser Leu Phe Tyr Leu Phe	
10 15 20	
TTC CTA GGC CTT GTG TAT GGG CAA CAA CCT ACG AAG ACT TCA AAT CCG	988
Phe Leu Gly Leu Val Tyr Gly Gln Gln Pro Thr Lys Thr Ser Asn Pro	
25 30 35	
AAC GAT CAG TGG ACC ATC AAA TGG AGT GCT TCG GAC GAA TTC AAC AAA	1036
Asn Asp Gln Trp Thr Ile Lys Trp Ser Ala Ser Asp Glu Phe Asn Lys	
40 45 50	
AAT GAC CCC GAC TGG GCA AAA TGG ATC AAG ACA GGA AAC CTT CCG AAT	1084
Asn Asp Pro Asp Trp Ala Lys Trp Ile Lys Thr Gly Asn Leu Pro Asn	
55 60 65 70	
ACA TCG GCA TGG AAA TGG AAC AAT CAA AAA AAC GTA AAG ATT TCC AAC	1132
Thr Ser Ala Trp Lys Trp Asn Asn Gln Lys Asn Val Lys Ile Ser Asn	
75 80 85	

GGA ATT GCG GAA CTA ACG ATG AGG CAT AAC GCC AAT AAT ACC CCA CCT	1180
Gly Ile Ala Glu Leu Thr Met Arg His Asn Ala Asn Asn Thr Pro Pro	
90 95 100	
GAC GGA GGA ACC TAT TTC ACC TCT GGG ATA TTT AAG TCG TAC CAA AAA	1228
Asp Gly Gly Thr Tyr Phe Thr Ser Gly Ile Phe Lys Ser Tyr Gln Lys	
105 110 115	
TTT ACG TAT GGA TAC TTT GAG GCC AAA ATC CAA GGA GCG GAT ATA GGT	1276
Phe Thr Tyr Gly Tyr Phe Glu Ala Lys Ile Gln Gly Ala Asp Ile Gly	
120 125 130	
GAA GGC GTA TGC CCA TCG TTT TGG CTT TAT AGT GAT TTC GAC TAT TCC	1324
Glu Gly Val Cys Pro Ser Phe Trp Leu Tyr Ser Asp Phe Asp Tyr Ser	
135 140 145 150	
GTA GCC AAT GGG GAA ACG GTA TAC AGT GAA ATA GAT GTA GTT GAA CTA	1372
Val Ala Asn Gly Glu Thr Val Tyr Ser Glu Ile Asp Val Val Glu Leu	
155 160 165	
CAA CAA TTC GAT TGG TAT GAA GGC CAT CAG GAC GAC ATT TAC GAC ATG	1420
Gln Gln Phe Asp Trp Tyr Glu Gly His Gln Asp Asp Ile Tyr Asp Met	
170 175 180	
GAC TTA AAT CTA CAC GCC GTT GTC AAA GAA AAC GGA CAG GGG GTT TGG	1468
Asp Leu Asn Leu His Ala Val Val Lys Glu Asn Gly Gln Gly Val Trp	
185 190 195	
AAA AGG CCA AAA ATG TAC CCT CAA GAA CAG TTG AAC AAA TGG AGA GCC	1516
Lys Arg Pro Lys Met Tyr Pro Gln Glu Gln Leu Asn Lys Trp Arg Ala	
200 205 210	
ATG GAC CCG AGT AAA GAC TTT CAT ATC TAT GGT TGT GAA GTG AAC CAG	1564
Met Asp Pro Ser Lys Asp Phe His Ile Tyr Gly Cys Glu Val Asn Gln	
215 220 225 230	
AAC GAA ATC ATA TGG TAT GTT GAC GGT GTC GAG GTT GCC CGA AAA CCA	1612
Asn Glu Ile Ile Trp Tyr Val Asp Gly Val Glu Val Ala Arg Lys Pro	
235 240 245	
AAT AAA TAT TGG CAT CGC CCC ATG AAC GTT ACC CTT TCA TTG GGA CTC	1660
Asn Lys Tyr Trp His Arg Pro Met Asn Val Thr Leu Ser Leu Gly Leu	
250 255 260	

AGA	AAA	CCA	TTT	GTG	AAA	TTT	TTC	GAC	AAT	AAG	AAC	AAT	GCC	ATA	AAT	1708
Arg	Lys	Pro	Phe	Val	Lys	Phe	Phe	Asp	Asn	Lys	Asn	Asn	Ala	Ile	Asn	
		265					270					275				
CCA	GAA	ACC	GAT	GCC	AAG	GCA	AGG	GAA	AAA	TTA	TCG	GAT	ATA	CCT	ACA	1756
Pro	Glu	Thr	Asp	Ala	Lys	Ala	Arg	Glu	Lys	Leu	Ser	Asp	Ile	Pro	Thr	
		280				285					290					
TCG	ATG	TAT	GTG	GAT	TAC	GTT	CGG	GTC	TGG	GAA	AAA	TCA	GCA	GGT	AAC	1804
Ser	Met	Tyr	Val	Asp	Tyr	Val	Arg	Val	Trp	Glu	Lys	Ser	Ala	Gly	Asn	
					300					305					310	
ACT	ACC	AAT	CCC	CCA	ACC	AGC	GAG	GTC	GGC	ACA	CTA	AAA	ACA	AAG	GGT	1852
Thr	Thr	Asn	Pro	Pro	Thr	Ser	Glu	Val	Gly	Thr	Leu	Lys	Thr	Lys	Gly	
				315					320						325	
TCG	AAA	CTG	GTG	ATT	GAC	CAT	TGG	GAT	GCA	AGT	ACA	GGG	ACT	ATT	TCG	1900
Ser	Lys	Leu	Val	Ile	Asp	His	Trp	Asp	Ala	Ser	Thr	Gly	Thr	Ile	Ser	
			330					335						340		
GCT	GTC	AGT	AAC	AAT	ACA	AAG	ACA	GGT	CAA	TAT	GCC	GGT	TCA	GTG	AAC	1948
Ala	Val	Ser	Asn	Asn	Thr	Lys	Thr	Gly	Gln	Tyr	Ala	Gly	Ser	Val	Asn	
		345					350					355				
AAC	GCG	AGC	ATC	GCC	CAG	ATA	GTA	ACA	TTA	AAA	GCG	AAT	ACT	TCA	TAT	1996
Asn	Ala	Ser	Ile	Ala	Gln	Ile	Val	Thr	Leu	Lys	Ala	Asn	Thr	Ser	Tyr	
		360				365					370					
AAG	GTA	TCG	GCT	TTC	GGA	AAG	GCC	AGC	TCA	CCC	GGA	ACA	TCG	GCT	TAT	2044
Lys	Val	Ser	Ala	Phe	Gly	Lys	Ala	Ser	Ser	Pro	Gly	Thr	Ser	Ala	Tyr	
					380					385					390	
CTA	GGC	ATT	AGT	AAA	GCA	TCC	AAC	AAC	GAA	CTC	ATA	AGC	AAT	TTT	GAA	2092
Leu	Gly	Ile	Ser	Lys	Ala	Ser	Asn	Asn	Glu	Leu	Ile	Ser	Asn	Phe	Glu	
				395					400						405	
TTC	AAA	ACA	ACC	TCA	TAC	TCC	AAA	GGC	GAG	ATT	GAG	ATA	AGA	ACT	GGA	2140
Phe	Lys	Thr	Thr	Ser	Tyr	Ser	Lys	Gly	Glu	Ile	Glu	Ile	Arg	Thr	Gly	
			410					415					420			
AAT	GTT	CAG	GAA	TCA	TAT	CGC	ATA	TGG	TAT	TGG	TCT	TCC	GGG	CAA	GCC	2188
Asn	Val	Gln	Glu	Ser	Tyr	Arg	Ile	Trp	Tyr	Trp	Ser	Ser	Gly	Gln	Ala	
		425					430					435				

TAT TGC GAT GAT TTT AAC CTT GTT GAA ATA AAC AGC GGG GCT TCA CAA 2236
 Tyr Cys Asp Asp Phe Asn Leu Val Glu Ile Asn Ser Gly Ala Ser Gln
 440 445 450

CTC AAT GAA AAT GAG ACT GAA ACA GCA CTG GAA AAA GGT ATA CAC ATT 2284
 Leu Asn Glu Asn Glu Thr Glu Thr Ala Leu Glu Lys Gly Ile His Ile
 455 460 465 470

TAT CCG AAT CCC TAT AAA AAC GGT CCA TTG ACA ATC GAT TTT GGC AAA 2332
 Tyr Pro Asn Pro Tyr Lys Asn Gly Pro Leu Thr Ile Asp Phe Gly Lys
 475 480 485

CCC TTC AGC GGC GAG GTC CAA ATC ACC GGT TTA AAC GGT AGA ACA TTC 2380
 Pro Phe Ser Gly Glu Val Gln Ile Thr Gly Leu Asn Gly Arg Thr Phe
 490 495 500

TTA AGA AGA AAT GTT GTC GAT CAA ACT TCG GTT CAG CTC CTA GAA TCC 2428
 Leu Arg Arg Asn Val Val Asp Gln Thr Ser Val Gln Leu Leu Glu Ser
 505 510 515

AAA TCT AAA TTC AAG AGC GGT CTA TAT ATC GTT AAA ATT AGT GGC CCG 2476
 Lys Ser Lys Phe Lys Ser Gly Leu Tyr Ile Val Lys Ile Ser Gly Pro
 520 525 530

GAT GGA GAG GTT TCA AAA AAG ATA CTC GTG GAG TAACTAAAAA TCAATTTTTA 2529
 Asp Gly Glu Val Ser Lys Lys Ile Leu Val Glu
 535 540 545

CAGGATTACA GACGGGCAAA GGGATTTTCC TTTGCCCGTT TTTAAAATTA TGGGCGGAAA 2589
 CGATTGTTGC G 2600

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Lys Lys Pro Asn Phe Tyr Gly Lys Met Gly Arg Thr Ala Leu Ser
 1 5 10 15
 Ser Leu Phe Tyr Leu Phe Phe Leu Gly Leu Val Tyr Gly Gln Gln Pro
 20 25 30

Thr	Lys	Thr	Ser	Asn	Pro	Asn	Asp	Gln	Trp	Thr	Ile	Lys	Trp	Ser	Ala	
		35						40								45
Ser	Asp	Glu	Phe	Asn	Lys	Asn	Asp	Pro	Asp	Trp	Ala	Lys	Trp	Ile	Lys	
	50					55					60					
Thr	Gly	Asn	Leu	Pro	Asn	Thr	Ser	Ala	Trp	Lys	Trp	Asn	Asn	Gln	Lys	
	65					70				75					80	
Asn	Val	Lys	Ile	Ser	Asn	Gly	Ile	Ala	Glu	Leu	Thr	Met	Arg	His	Asn	
				85					90					95		
Ala	Asn	Asn	Thr	Pro	Pro	Asp	Gly	Gly	Thr	Tyr	Phe	Thr	Ser	Gly	Ile	
			100					105					110			
Phe	Lys	Ser	Tyr	Gln	Lys	Phe	Thr	Tyr	Gly	Tyr	Phe	Glu	Ala	Lys	Ile	
		115					120					125				
Gln	Gly	Ala	Asp	Ile	Gly	Glu	Gly	Val	Cys	Pro	Ser	Phe	Trp	Leu	Tyr	
	130					135					140					
Ser	Asp	Phe	Asp	Tyr	Ser	Val	Ala	Asn	Gly	Glu	Thr	Val	Tyr	Ser	Glu	
145					150					155					160	
Ile	Asp	Val	Val	Glu	Leu	Gln	Gln	Phe	Asp	Trp	Tyr	Glu	Gly	His	Gln	
				165					170					175		
Asp	Asp	Ile	Tyr	Asp	Met	Asp	Leu	Asn	Leu	His	Ala	Val	Val	Lys	Glu	
		180					185						190			
Asn	Gly	Gln	Gly	Val	Trp	Lys	Arg	Pro	Lys	Met	Tyr	Pro	Gln	Glu	Gln	
	195					200						205				
Leu	Asn	Lys	Trp	Arg	Ala	Met	Asp	Pro	Ser	Lys	Asp	Phe	His	Ile	Tyr	
	210					215					220					
Gly	Cys	Glu	Val	Asn	Gln	Asn	Glu	Ile	Ile	Trp	Tyr	Val	Asp	Gly	Val	
225					230					235					240	
Glu	Val	Ala	Arg	Lys	Pro	Asn	Lys	Tyr	Trp	His	Arg	Pro	Met	Asn	Val	
				245					250					255		
Thr	Leu	Ser	Leu	Gly	Leu	Arg	Lys	Pro	Phe	Val	Lys	Phe	Phe	Asp	Asn	
			260				265						270			
Lys	Asn	Asn	Ala	Ile	Asn	Pro	Glu	Thr	Asp	Ala	Lys	Ala	Arg	Glu	Lys	
	275						280					285				
Leu	Ser	Asp	Ile	Pro	Thr	Ser	Met	Tyr	Val	Asp	Tyr	Val	Arg	Val	Trp	
	290					295					300					
Glu	Lys	Ser	Ala	Gly	Asn	Thr	Thr	Asn	Pro	Pro	Thr	Ser	Glu	Val	Gly	
305					310					315					320	
Thr	Leu	Lys	Thr	Lys	Gly	Ser	Lys	Leu	Val	Ile	Asp	His	Trp	Asp	Ala	
				325					330					335		
Ser	Thr	Gly	Thr	Ile	Ser	Ala	Val	Ser	Asn	Asn	Thr	Lys	Thr	Gly	Gln	
		340						345					350			
Tyr	Ala	Gly	Ser	Val	Asn	Asn	Ala	Ser								

Leu	Ile	Ser	Asn	Phe	Glu	Phe	Lys	Thr	Ser	Tyr	Ser	Lys	Gly	Glu		
405								410				415				
Ile	Glu	Ile	Arg	Thr	Gly	Asn	Val	Gln	Glu	Ser	Tyr	Arg	Ile	Trp	Tyr	
420								425				430				
Trp	Ser	Ser	Gly	Gln	Ala	Tyr	Cys	Asp	Asp	Phe	Asn	Leu	Val	Glu	Ile	
435							440				445					
Asn	Ser	Gly	Ala	Ser	Gln	Leu	Asn	Glu	Asn	Glu	Thr	Glu	Thr	Ala	Leu	
450						455				460						
Glu	Lys	Gly	Ile	His	Ile	Tyr	Pro	Asn	Pro	Tyr	Lys	Asn	Gly	Pro	Leu	
465					470				475					480		
Thr	Ile	Asp	Phe	Gly	Lys	Pro	Phe	Ser	Gly	Glu	Val	Gln	Ile	Thr	Gly	
485								490				495				
Leu	Asn	Gly	Arg	Thr	Phe	Leu	Arg	Arg	Asn	Val	Val	Asp	Gln	Thr	Ser	
500							505				510					
Val	Gln	Leu	Leu	Glu	Ser	Lys	Ser	Lys	Phe	Lys	Ser	Gly	Leu	Tyr	Ile	
515						520				525						
Val	Lys	Ile	Ser	Gly	Pro	Asp	Gly	Glu	Val	Ser	Lys	Lys	Ile	Leu	Val	
530						535				540						
Glu																
545																